SEQUENCE LISTING

						_											
5	<110>	Duke Chuan Xiuwu	-Yua	n, L	ty i												
	<120>	GENER COMPL	ATIO	N OF ADEN	RECO OVIR	OMBI US-M	NANT EDIA	ADE TED	NO-A APPR	SSOC OACH	IATE	D VI	RAL	VECT	ORS :	BY A	
10	<130>	180/1	37														
	<150> <151>																
15	<160>	22															
	<170>	Paten	tIn	vers	ion	3.2											
20	<210> <211> <212> <213>	1611 DNA	-ass	ocia	ted	viru	.s 2										
25	<220> <221> <222>		(161	.1)													
30	<400> atg co Met Pr 1	1 cg ggg ro Gly	ttt Phe	tac Tyr 5	gag Glu	att Ile	gtg Val	att Ile	aag Lys 10	gtc Val	ccc Pro	agc Ser	gac Asp	ctt Leu 15	gac Asp		48
35	gag ca Glu H	at ctg is Leu	ccc Pro 20	ggc Gly	att Ile	tct Ser	gac Asp	agc Ser 25	ttt Phe	gtg Val	aac Asn	tgg Trp	gtg Val 30	gcc Ala	gag Glu		96
40	aag g Lys G	aa tgg lu Trp 35	gag Glu	ttg Leu	ccg Pro	cca Pro	gat Asp 40	tct Ser	gac Asp	atg Met	gat Asp	ctg Leu 45	aat Asn	ctg Leu	att Ile		144
	gag c Glu G 5	ag gca ln Ala 0	ccc Pro	ctg Leu	acc Thr	gtg Val 55	gcc Ala	gag Glu	aag Lys	ctg Leu	cag Gln 60	cgc Arg	gac Asp	ttt Phe	ctg Leu		192
45	acg g Thr G 65	aa tgg lu Trp	cgc Arg	cgt Arg	gtg Val 70	agt Ser	aag Lys	gcc Ala	ccg Pro	gag Glu 75	gcc Ala	ctt Leu	ttc Phe	ttt Phe	gtg Val 80		240
50	caa t Gln P	tt gag he Glu	aag Lys	gga Gly 85	gag Glu	agc Ser	tac Tyr	ttc Phe	cac His 90	atg Met	cac His	gtg Val	ctc Leu	gtg Val 95	gaa Glu		288
55	acc a Thr T	.cc ggg hr Gly	gtg Val 100	aaa Lys	tcc Ser	atg Met	gtt Val	ttg Leu 105	gga Gly	cgt Arg	ttc Phe	ctg Leu	agt Ser 110	cag Gln	att Ile		336
60	cgc g Arg G	aa aaa Slu Lys 115	Leu	att Ile	cag Gln	aga Arg	att Ile 120	tac Tyr	cgc Arg	Gly ggg	atc Ile	gag Glu 125	ccg Pro	act Thr	ttg Leu		384
	Pro A	ac tgg sn Trp .30	ttc Phe	gcg Ala	gtc Val	aca Thr 135	aag Lys	acc Thr	aga Arg	aat Asn	ggc Gly 140	gcc Ala	gga Gly	ggc Gly	Gly		432

_	aac Asn 145	aag Lys	gtg Val	gtg Val	gat Asp	gag Glu 150	tgc Cys	tac Tyr	atc Ile	ccc Pro	aat Asn 155	tac Tyr	ttg Leu	ctc Leu	ccc Pro	aaa Lys 160	480
5	acc Thr	cag Gln	cct Pro	gag Glu	ctc Leu 165	cag Gln	tgg Trp	gcg Ala	tgg Trp	act Thr 170	aat Asn	atg Met	gaa Glu	cag Gln	tat Tyr 175	tta Leu	528
10	agc Ser	gcc Ala	tgt Cys	ttg Leu 180	aat Asn	ctc Leu	acg Thr	gag Glu	cgt Arg 185	aaa Lys	cgg Arg	ttg Leu	gtg Val	gcg Ala 190	cag Gln	cat His	576
15	ctg Leu	acg Thr	cac His 195	gtg Val	tcg Ser	cag Gln	acg Thr	cag Gln 200	gag Glu	cag Gln	aac Asn	aaa Lys	gag Glu 205	aat Asn	cag Gln	aat Asn	624
20	ccc Pro	aat Asn 210	tct Ser	gat Asp	gcg Ala	ccg Pro	gtg Val 215	atc Ile	aga Arg	tca Ser	aaa Lys	act Thr 220	tca Ser	gcc Ala	agg Arg	tac Tyr	672
25	atg Met 225	gag Glu	ctg Leu	gtc Val	Gly ggg	tgg Trp 230	ctc Leu	gtg Val	gac Asp	aag Lys	ggg Gly 235	att Ile	acc Thr	tcg Ser	gag Glu	aag Lys 240	720
25	cag Gln	tgg Trp	atc Ile	cag Gln	gag Glu 245	gac Asp	cag Gln	gcc Ala	tca Ser	tac Tyr 250	atc Ile	tcc Ser	ttc Phe	aat Asn	gcg Ala 255	gcc Ala	768
30	tcc Ser	aac Asn	tcg Ser	cgg Arg 260	tcc Ser	caa Gln	atc Ile	aag Lys	gct Ala 265	gcc Ala	ttg Leu	gac Asp	aat Asn	gcg Ala 270	gga Gly	aag Lys	816
35	att Ile	atg Met	agc Ser 275	Leu	act Thr	aaa Lys	acc Thr	gcc Ala 280	Pro	gac Asp	tac Tyr	ctg Leu	gtg Val 285	ggc Gly	cag Gln	cag Gln	864
40	ccc Pro	gtg Val 290	Glu	gac Asp	att Ile	tcc Ser	agc Ser 295	Asn	cgg Arg	att Ile	tat Tyr	aaa Lys 300	He	ttg Leu	gaa Glu	cta Leu	912
45	aac Asn 305	Gly	tac Tyr	gat Asp	ccc Pro	caa Gln 310	tat Tyr	gcg Ala	gct Ala	tcc Ser	gtc Val 315	ttt Phe	ctg Leu	gga Gly	tgg Trp	gcc Ala 320	960
45	acg Thr	aaa Lys	aag Lys	ttc Phe	ggc Gly 325	Lys	agg Arg	aac Asn	acc Thr	atc Ile 330	Trp	ctg Leu	ttt Phe	ggg	cct Pro 335	gca Ala	1008
50	act Thr	acc Thr	ggg Gly	aag Lys 340	Thr	Asn	Ile	: Ala	Glu	Ala	Ile	Ala	cac His	Tur	. var	ccc Pro	1056
55	ttc Phe	tac Tyr	ggg Gly 355	Cys	gta Val	aac . Asn	tgg Trp	acc Thr 360	Asn	gag Glu	aac Asn	ttt Phe	ccc Pro 365	Pne	aac Asr	gac Asp	1104
60	tgt Cys	gto Val 370	. Asr	aag Lys	g atg Met	gtg Val	ato Ile 375	rrr:	tgg Trp	gag Glu	gag Glu	ggg Gly 380	гLys	atg Met	aco Thi	gcc Ala	1152
	aag Lys 385	: Val	gtg L Val	g gag L Glu	j tog i Sei	gcc Ala 390	Lys	gco Ala	att Ile	cto Lev	gga Gly 395	r Gl	ago Ser	aaç Lys	g gtg Val	g cgc L Arg 400	1200

e	gtg Val	gac Asp	cag Gln	aaa Lys	tgc Cys 405	aag Lys	tcc Ser	tcg Ser	gcc Ala	cag Gln 410	ata Ile	gac Asp	ccg Pro	act Thr	ccc Pro 415	gtg Val	1248
5	atc Ile	gtc Val	acc Thr	tcc Ser 420	aac Asn	acc Thr	aac Asn	atg Met	tgc Cys 425	gcc Ala	gtg Val	att Ile	gac Asp	ggg Gly 430	aac Asn	tca Ser	1296
10	acg Thr	acc Thr	ttc Phe 435	gaa Glu	cac His	cag Gln	cag Gln	ccg Pro 440	ttg Leu	caa Gln	gac Asp	cgg Arg	atg Met 445	ttc Phe	aaa Lys	ttt Phe	1344
15	gaa Glu	ctc Leu 450	acc Thr	cgc Arg	cgt Arg	ctg Leu	gat Asp 455	cat His	gac Asp	ttt Phe	GJA aaa	aag Lys 460	gtc Val	acc Thr	aag Lys	cag Gln	1392
20	gaa Glu 465	gtc Val	aaa Lys	gac Asp	ttt Phe	ttc Phe 470	cgg Arg	tgg Trp	gca Ala	aag Lys	gat Asp 475	cac His	gtg Val	gtt Val	gag Glu	gtg Val 480	1440
25	gag Glu	cat His	gaa Glu	ttc Phe	tac Tyr 485	gtc Val	aaa Lys	aag Lys	ggt Gly	gga Gly 490	gcc Ala	aag Lys	aaa Lys	aga Arg	ccc Pro 495	gcc Ala	1488
25	ccc Pro	agt Ser	gac Asp	gca Ala 500	Asp	ata Ile	agt Ser	gag Glu	ccc Pro 505	aaa Lys	cgg Arg	gtg Val	cgc Arg	gag Glu 510	tca Ser	gtt Val	1536
30	gcg Ala	cag Gln	cca Pro 515	Ser	acg Thr	tca Ser	gac Asp	gcg Ala 520	gaa Glu	gct Ala	tcg Ser	atc Ile	aac Asn 525	tac Tyr	gca Ala	gac Asp	1584
35	aga Arg	ttg Leu 530	Ala	cga Arg	gga Gly	cac His	tct Ser 535	ctc Leu	tga								1611
40	<21 <21 <21 <21	1> 2>	2 536 PRT aden	o-as	soci	ated	vir	us 2									
45	<40		2														
45	Met 1	Pro	Gly	Phe	Tyr 5	Glu	Ile	Val	Ile	Lys 10	Val	. Pro	, Ser	Asp	15	Asp	
50	Glu	His	Leu	Pro 20	Gly	'Ile	Ser	Asp	Ser 25	Phe	Val	. Asr	Trp	Val 30	Ala	Glu	
55	Lys	Glu	Trp 35	Glu	ı Lev	Pro	Pro	Asr 40	Ser	Asp	Met	. Asp	45	Asn	ı Leı	ılle	
60	Glu	50 50	n Ala	a Pro	Let	ı Thr	Val	. Ala	ı Glı	Lys	: Lev	Glr 60	Arg	, yst	Phe	e Leu	
	Thi 65	Glı	ı Try) Arg	y Arg	y Val 70	. Ser	Lys	a Ala	Pro	75	ı Alá	ı Lev	ı Phe	e Pho	e Val 80	

	Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu
5	Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile
10	Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
15	Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly
20	Asn 145	Lys	Val	Val	Asp	Glu 150	Суз	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
	Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu
25	Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His
30	Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
35	Pro	Asn 210		Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr
40	Met 225	Glu	Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240
	Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Туг 250	Ile	Ser	Phe	Asn	Ala 255	Ala
45	Ser	Asn	Ser	Arg 260		Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys
50	Ile	Met	Ser 275		Thr	. Lys	Thr	Ala 280	Pro) Asp	Tyr	Leu	Val 285	Gly	Gln	Gln
55	Pro	Val 290		ı Asp	Ile	. Ser	Ser 295	Asn	Arg	, Il∈	туг	100 300	Ile	. Leu	Glu	Leu
60	Asn 305		туг	asp	Pro	310		: Ala	. Ala	a Sei	7 Val 315	Phe	. Lev	Gly	Tr	Ala 320
	Thr	Lys	Lys	s Phe	Gly 325		Arg	, Asn	Thi	330		Leu	Phe	e Gly	9rc 335	Ala

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro

- 5 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
- Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 10
- Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 15
- Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 20
 - Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
- 25 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
- Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 30
- Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 35
- Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 49540
 - Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
- 45 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
- Arg Leu Ala Arg Gly His Ser Leu 50
- <211> 1866 <212> DNA 55

 - <213> adeno-associated virus 2
- ′ <220> <221> CDS <222> (1)..(1866) <400> 3

	atg Met 1	ccg Pro	Gly ggg	ttt Phe	tac Tyr 5	gag Glu	att Ile	gtg Val	att Ile	aag Lys 10	gtc Val	ccc Pro	agc Ser	gac Asp	ctt Leu 15	gac Asp	48
5	G1A aaa	cat His	ctg Leu	ccc Pro 20	ggc Gly	att Ile	tct Ser	gac Asp	agc Ser 25	ttt Phe	gtg Val	aac Asn	tgg Trp	gtg Val 30	gcc Ala	gag Glu	96
10	aag Lys	gaa Glu	tgg Trp 35	gag Glu	ttg Leu	ccg Pro	cca Pro	gat Asp 40	tct Ser	gac Asp	atg Met	gat Asp	ctg Leu 45	aat Asn	ctg Leu	att Ile	144
15	gag Glu	cag Gln 50	gca Ala	ccc Pro	ctg Leu	acc Thr	gtg Val 55	gcc Ala	gag Glu	aag Lys	ctg Leu	cag Gln 60	cgc Arg	gac Asp	ttt Phe	ctg Leu	192
20	acg Thr 65	gaa Glu	tgg Trp	cgc Arg	cgt Arg	gtg Val 70	agt Ser	aag Lys	gcc Ala	ccg Pro	gag Glu 75	gcc Ala	ctt Leu	ttc Phe	ttt Phe	gtg Val 80	240
20	caa Gln	ttt Phe	gag Glu	aag Lys	gga Gly 85	gag Glu	agc Ser	tac Tyr	ttc Phe	cac His 90	atg Met	cac His	gtg Val	ctc Leu	gtg Val 95	gaa Glu	288
25	acc Thr	acc Thr	Gly	gtg Val 100	aaa Lys	tcc Ser	atg Met	gtt Val	ttg Leu 105	gga Gly	cgt Arg	ttc Phe	ctg Leu	agt Ser 110	cag Gln	att Ile	336
30	cgc Arg	gaa Glu	aaa Lys 115	ctg Leu	att Ile	cag Gln	aga Arg	att Ile 120	Tyr	cgc Arg	ggg	atc Ile	gag Glu 125	ccg Pro	act Thr	ttg Leu	384
35	cca Pro	aac Asn 130	Trp	ttc Phe	gcg Ala	gtc Val	aca Thr 135	Lys	acc Thr	aga Arg	aat Asn	ggc Gly 140	gcc Ala	gga Gly	ggc	ggg	432
40	aac Asn 145	Lys	gtg Val	gtg Val	gat Asp	gag Glu 150	tgc Cys	tac Tyr	atc Ile	ccc Pro	aat Asn 155	Tyr	ttg Leu	ctc Leu	ccc Pro	aag Lys 160	480
40	acc Thr	cag Gln	cct Pro	gaa Glu	ctg Leu 165	Gln	tgg Trp	gcg Ala	tgg Trp	act Thr 170	Asn	atg Met	gaa Glu	cag Gln	tat Tyr 175	tta Leu	528
45	agc Ser	gcc Ala	tgt Cys	ttg Leu 180	Asn	ctc Leu	acg Thr	gag Glu	cgt Arg 185	Lys	. cgg Arg	ttg Leu	gtg Val	gcg Ala 190	GID	cat His	576
50	ctg Leu	acg Thr	cac His	: Val	tcg Ser	cag Gln	acg Thr	cag Gln 200	Glu	cag Gln	aac Asn	aaa Lys	gag Glu 205	Asn	cag Gln	aat Asn	624
55	ccc Pro	aat Asn 210	ı Ser	gat Asp	gcg Ala	ccg Pro	gtg Val 215	. Ile	aga Arg	tca Ser	aaa Lys	act Thr 220	Ser	gco Ala	agg Arg	tac Tyr	672
	atg Met 225	Glu	g ctg ı Lev	gto Val	Gly Gly	tgg Trp 230	Let	gtg Val	gac Asp	aag Lys	ggg Gly 235	, ITE	acc Thr	tcg Ser	gag Glu	aag Lys 240	720
60	cag Gln	tgg Tr	g ata o Ile	cag Glr	g gag 1 Glu 245	ı Asp	cag Glr	g gcc Ala	tca Sei	tac Tyr 250	: TTE	tco Ser	tto Phe	aat Asr	gcg Ala 255	gcc Ala	768

	tcc Ser	aac Asn	tcg Ser	cgg Arg 260	tcc Ser	caa Gln	atc Ile	aag Lys	gct Ala 265	gcc Ala	ttg Leu	gac Asp	aat Asn	gcg Ala 270	gga Gly	aag Lys	816
5	att Ile	atg Met	agc Ser 275	ctg Leu	act Thr	aaa Lys	acc Thr	gcc Ala 280	ccc Pro	gac Asp	tac Tyr	ctg Leu	gtg Val 285	ggc Gly	cag Gln	cag Gln	864
10	ccc Pro	gtg Val 290	gag Glu	gac Asp	att Ile	tcc Ser	agc Ser 295	aat Asn	cgg Arg	att Ile	tat Tyr	aaa Lys 300	att Ile	ttg Leu	gaa Glu	cta Leu	912
15	aac Asn 305	ggg Gly	tac Tyr	gat Asp	ccc Pro	caa Gln 310	tat Tyr	gcg Ala	gct Ala	tcc Ser	gtc Val 315	ttt Phe	ctg Leu	gga Gly	tgg Trp	gcc Ala 320	960
20	acg Thr	aaa Lys	aag Lys	ttc Phe	ggc Gly 325	aag Lys	agg Arg	aac Asn	acc Thr	atc Ile 330	tgg Trp	ctg Leu	ttt Phe	GJA aaa	cct Pro 335	gca Ala	1008
20	act Thr	acc Thr	ggg Gly	aag Lys 340	acc Thr	aac Asn	atc Ile	gcg Ala	gag Glu 345	gcc Ala	ata Ile	gcc Ala	cac His	act Thr 350	gtg Val	ccc Pro	1056
25	ttc Phe	tac Tyr	ggg Gly 355	tgc Cys	gta Val	aac Asn	tgg Trp	acc Thr 360	aat Asn	gag Glu	aac Asn	ttt Phe	ccc Pro 365	ttc Phe	aac Asn	gac Asp	1104
30	tgt Cys	gtc Val 370	gat Asp	aag Lys	atg Met	gtg Val	atc Ile 375	tgg Trp	tgg Trp	gag Glu	gag Glu	ggg Gly 380	aag Lys	atg Met	acc Thr	gcc Ala	1152
35	aag Lys 385	gtc Val	gtg Val	gag Glu	tcg Ser	gcc Ala 390	aaa Lys	gcc Ala	att Ile	ctc Leu	gga Gly 395	Gly	agc Ser	aag Lys	gtg Val	cgc Arg 400	1200
40	gtg Val	gac Asp	cag Gln	aaa Lys	tgc Cys 405	aag Lys	tcc Ser	tcg Ser	gcc Ala	cag Gln 410	ata Ile	gac Asp	ccg Pro	act Thr	ccc Pro 415	gtg Val	1248
40 .	atc Ile	gtc Val	acc Thr	tcc Ser 420	aac Asn	acc Thr	aat Asn	atg Met	tgc Cys 425	Ala	gtg Val	att Ile	gac Asp	ggg Gly 430	Asn	tca Ser	1296
45	acg Thr	acc Thr	ttc Phe 435	Glu	cac His	cag Gln	cag Gln	ccg Pro 440	Leu	caa Gln	gac Asp	cgg Arg	atg Met 445	Pne	aaa Lys	ttt Phe	1344
50	gaa Glu	ctc Leu 450	Thr	cgc Arg	cgt Arg	ctg Leu	gat Asp 455	His	gac Asp	ttt Phe	Gly	aag Lys 460	Val	acc Thr	aag Lys	cag Gln	1392
55	gaa Glu 465	Val	aaa Lys	gac Asp	ttt Phe	ttc Phe 470	Arg	tgg Trp	gca Ala	aag Lys	gat Asp 475	His	gtg Val	gtt Val	gag Glu	gtg Val 480	1440
Ω	gag Glu	cat	gag Glu	ttc Phe	tac Tyr 485	· Val	aaa Lys	aag Lys	ggt Gly	gga Gly 490	Ala	aag Lys	aaa Lys	aga Arg	Pro 495	Ala	1488
60	ccc Pro	agt Ser	gac Asp	gca Ala 500	gat Asp	ata Ile	agt Ser	gag Glu	r ccc Pro 505) Lys	cgg Arg	gtg Val	. Arg	gag Glu 510	Ser	gtt Val	1536

	gcg Ala	cag Gln	cca Pro 515	tcg Ser	acg Thr	tca Ser	gac Asp	gcg Ala 520	gaa Glu	gct Ala	tcg Ser	atc Ile	aac Asn 525	tac Tyr	gca Ala	gat Asp	1584
5	aga Arg	tac Tyr 530	caa Gln	aac Asn	aaa Lys	tgt Cys	tct Ser 535	cgt Arg	cac His	gtg Val	ggc Gly	atg Met 540	aat Asn	ctg Leu	atg Met	ctg Leu	1632
10	ttt Phe 545	ccg Pro	tgc Cys	aga Arg	caa Gln	tgc Cys 550	gag Glu	aga Arg	atg Met	aat Asn	cag Gln 555	aac Asn	tca Ser	aat Asn	atc Ile	tgc Cys 560	1680
15	ttc Phe	act Thr	cac His	gga Gly	cag Gln 565	aaa Lys	gac Asp	tgt Cys	tta Leu	gag Glu 570	tgc Cys	ttt Phe	ccc Pro	gtg Val	tca Ser 575	gaa Glu	1728
20	tct Ser	caa Gln	ccc Pro	gtt Val 580	tct Ser	gtc Val	gtc Val	aaa Lys	aag Lys 585	gcg Ala	tat Tyr	cag Gln	aaa Lys	ctg Leu 590	tgc Cys	tac Tyr	1776
20	att Ile	cat His	cat His 595	atc Ile	atg Met	gga Gly	aag Lys	gtg Val 600	cca Pro	gac Asp	gct Ala	tgc Cys	act Thr 605	gcc Ala	tgc Cys	gat Asp	1824
25	ctg Leu	gtc Val 610	Asn	gtg Val	gat Asp	ttg Leu	gat Asp 615	gac Asp	tgc Cys	atc Ile	ttt Phe	gaa Glu 620	caa Gln	taa			1866
30	<21 <21 <21 <21	1> 2>	4 621 PRT aden	o-as:	soci	ated	vir	us 2									
35	<40	0>	4														
	Met 1	Pro	Gly	Phe	Tyr 5	Glu	Ile	Val	Ile	Lys 10	Val	Pro	Ser	Asp	Leu 15	Asp	
4.0	Gly	His	Leu	Pro 20	Gly	Ile	Ser	Asp	Ser 25	Phe	Val	Asn	Trp	Val 30	Ala	Glu	
45	Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp 40	Ser	Asp	Met	Asp	Leu 45	Asn	Leu	Ile	
50	Glu	Gln 50	Ala	Pro	Leu	Thr	Val 55	Ala	Glu	Lys	Leu	Gln 60	Arg	Asp	Phe	Leu	
55	Thr 65	Glu	Trp	Arg	Arg	70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80	
	Gln	Ph∈	Glu	Lys		r Glu	Ser	Туг	Phe	His	Met	: His	val	Let	ı Val 95	Glu	
					85					90					•		

	Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
5	Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly
10	Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
15	Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	туr 175	Leu
	Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His
20	Leu	Thr	His 195		Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
25	Pro	Asn 210		Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Тут
30	Met 225		Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lуз 240
35	Gln	Trp	Ile	Gln	Glu 245		Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala
	Ser	Asn	Ser	Arg 260		Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys
40	Ile	Met	Ser 275		Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285	Gly	Gln	Glı
45	Pro	Val 290		. Asp	Ile	Ser	Ser 295	Asn	Arg	Ile	. Tyr	300	; Ile	Leu	. Glu	Le
50	Asn 305		у Туг	Asp	Pro	Gln 310	тух)	: Ala	Ala	Ser	7 Val	Phe	e Leu	Gly	Trp	Ala 32
55	Thr	· Lys	. Lys	s Ph∈	Gly 325		arg	J Asr	Thr	330	e Trp	Let	ı Phe	: Gly	9rc 335	Al

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355

60

	Cys	Val 370	Asp	Lys	Met	Val	11e 375	Trp	Trp	Glu	Glu	380	Lys	Met	Thr	Ala
5	Lys 385	Val	Val	Glu	Ser	Ala 390	Lys	Ala	Ile	Leu	Gly 395	Gly	Ser	Lys	Val	Arg 400
10	Val	Asp	Gln	Lys	Суз 405	Lys	Ser	Ser	Ala	Gln 410	Ile	Asp	Pro	Thr	Pro 415	Val
15	Ile	Val	Thr	Ser 420	Asn	Thr	Asn	Met	Cys 425	Ala	Val	Ile	Asp	Gly 430	Asn	Ser
	Thr	Thr	Phe 435	Glu	His	Gln	Gln	Pro 440	Leu	Gln	Asp	Arg	Met 445	Phe	Lys	Phe
20	Glu	Leu 450		Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Ьуs 460	Val	Thr	Lys	Gln
25	Glu 465	Val	Lys	Asp	Phe	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu	Val 480
30	Glu	His	Glu	Phe	Tyr 485	Val	Lys	Lys	Gly	Gly 490	Ala	Lys	Lys	Arg	Pro 495	Ala
35	Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu 510	Ser	Val
	Ala	Gln	Pro 515		Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn 525	Tyr	Ala	Asp
40	Arg	Tyr 530		Asn	Lys	Cys	Ser 535	Arg	His	Val	Gly	Met 540	Asn	Leu	Met	Leu
45	Phe 545		Суз	Arg	Gln	Cys 550		Arg	Met	Asn	Gln 555	Asn	Ser	Asn	Ile	Су: 560
50	Phe	Thr	His	Gly	Gln 565	Lys	Asp	Cys	Leu	Glu 570	Суз	Phe	Pro	Val	Ser 575	Glı
55	Ser	Gln	Pro	Val 580		Val	Val	Lys	Lys 585	Ala	Tyr	Gln	Lys	Leu 590	Cys	TY
	Ile	His	His 595		Met	Gly	Lys	Val 600		Asp	Ala	Суя	Thr 605	Ala	Cys	As
60	Leu	Val 610		Val	. Asp	Leu	Asp 615		Cys	: Ile	Phe	Glu 620	Gln	<u>L</u>		

<210>

3574 <211> <212> DNA <213> adeno-associated virus 2 5 <400> 5 acggttggtg gcgcagcatc tgacgcacgt gtcgcagacg caggagcaga acaaagagaa 60 tcagaatccc aattctgatg cgccggtgat cagatcaaaa acttcagcca ggtacatgga 120 10 180 gctggtcggg tggctcgtgg acaaggggat tacctcggag aagcagtgga tccaggagga ccaggcctca tacatctcct tcaatgcggc ctccaactcg cggtcccaaa tcaaggctgc 240 cttggacaat gcgggaaaga ttatgagcct gactaaaacc gcccccgact acctggtggg 300 15 ccagcagccc gtggaggaca tttccagcaa tcggatttat aaaattttgg aactaaacgg 360 gtacgatccc caatatgcgg cttccgtctt tctgggatgg gccacgaaaa agttcggcaa 420 20 480 gaggaacacc atctggctgt ttgggcctgc aactaccggg aagaccaaca tcgcggaggc catageceae actgtgeeet tetaegggtg egtaaactgg accaatgaga acttteeett 540 caacgactgt gtcgacaaga tggtgatctg gtgggaggag gggaagatga ccgccaaggt 600 25 cgtggagtcg gccaaagcca ttctcggagg aagcaaggtg cgcgtggacc agaaatgcaa 660 gtcctcggcc cagatagacc cgactcccgt gatcgtcacc tccaacacca acatgtgcgc 720 30 780 cgtgattgac gggaactcaa cgaccttcga acaccagcag ccgttgcaag accggatgtt 840 caaatttgaa ctcacccgcc gtctggatca tgactttggg aaggtcacca agcaggaagt caaagacttt ttccggtggg caaaggatca cgtggttgag gtggagcatg aattctacgt 900 35 caaaaagggt ggagccaaga aaagacccgc ccccagtgac gcagatataa gtgagcccaa 960 acgggtgcgc gagtcagttg cgcagccatc gacgtcagac gcggaagctt cgatcaacta 1020 40 1080 cgcagacagg taccaaaaca aatgtteteg teacgtgggc atgaatetga tgetgtttee 1140 ctgcagacaa tgcgagagaa tgaatcagaa ttcaaatatc tgcttcactc acggacagaa agactgttta gagtgctttc ccgtgtcaga atctcaaccc gtttctgtcg tcaaaaaggc 1200 45 1260 gtatcagaaa ctgtgctaca ttcatcatat catgggaaag gtgccagacg cttgcactgc ctgcgatctg gtcaatgtgg atttggatga ctgcatcttt gaacaataaa tgatttaaat 1320 50 caggtatggc tgccgatggt tatcttccag attggctcga ggacactctc tctgaaggaa 1380 1440 taagacagtg gtggaagete aaacetggee caccaccace aaageeegea gageggeata aggacgacag caggggtett gtgetteetg ggtacaagta ceteggacee tteaacggac 1500 55 tcgacaaggg agagccggtc aacgaggcag acgccgcggc cctcgagcac gacaaagcct 1560 acgaccggca gctcgacagc ggagacaacc cgtacctcaa gtacaaccac gccgacgcgg 1620 60 1680 agtttcagga gcgccttaaa gaagatacgt cttttggggg caacctcgga cgagcagtct tccaggcgaa aaagagggtt cttgaacctc tgggcctggt tgaggaacct gttaagacgg 1740

	ctccgggaaa	aaagaggccg	gtagagcact	ctcctgtgga	gccagactcc	tcctcgggaa	1800
	ccggaaaggc	gggccagcag	cctgcaagaa	aaagattgaa	ttttggtcag	actggagacg	1860
5	cagactcagt	acctgacccc	cagcctctcg	gacagccacc	agcagccccc	tctggtctgg	1920
	gaactaatac	gatggctaca	ggcagtggcg	caccaatggc	agacaataac	gagggcgccg	1980
	acggagtggg	taattcctcg	ggaaattggc	attgcgattc	cacatggatg	ggcgacagag	2040
10	tcatcaccac	cagcacccga	acctgggccc	tgcccaccta	caacaaccac	ctctacaaac	2100
	aaatttccag	ccaatcagga	gcctcgaacg	acaatcacta	ctttggctac	agcacccctt	2160
15	gggggtattt	tgacttcaac	agattccact	gccacttttc	accacgtgac	tggcaaagac	2220
	tcatcaacaa	caactgggga	ttccgaccca	agagactcaa	cttcaagctc	tttaacattc	2280
	aagtcaaaga	ggtcacgcag	aatgacggta	cgacgacgat	tgccaataac	cttaccagca	2340
20	cggttcaggt	gtttactgac	teggagtace	agctcccgta	cgtcctcggc	teggegeate	2400
	aaggatgcct	cccgccgttc	ccagcagacg	tcttcatggt	gccacagtat	ggatacctca	2460
25	ccctgaacaa	cgggagtcag	gcagtaggac	gctcttcatt	ttactgcctg	gagtactttc	2520
	cttctcagat	gctgcgtacc	ggaaacaact	ttaccttcag	ctacactttt	gaggacgttc	2580
	ctttccacag	cagctacgct	cacagccaga	gtctggaccg	tctcatgaat	cctctcatcg	2640
30	accagtacct	gtattacttg	agcagaacaa	acactccaag	tggaaccacc	acgcagtcaa	2700
	ggcttcagtt	ttctcaggcc	ggagcgagtg	acattcggga	ccagtctagg	aactggcttc	2760
35	ctggaccctg	ttaccgccag	cagcgagtat	caaagacatc	tgcggataac	aacaacagtg	2820
	aatactcgtg	gactggagct	accaagtacc	acctcaatgg	cagagactct	ctggtgaatc	2880
	cgggcccggc	catggcaagc	cacaaggacg	atgaagaaaa	gttttttcct	cagagcgggg	2940
40	ttctcatctt	tgggaagcaa	ggctcagaga	aaacaaatgt	ggacattgaa	aaggtcatga	3000
	ttacagacga	agaggaaatc	aggacaacca	atcccgtggc	tacggagcag	tatggttctg	3060
45	tatctaccaa	cctccagaga	ggcaacagac	aagcagctac	cgcagatgtc	aacacacaag	3120
	gcgttcttcc	aggcatggtc	tggcaggaca	gagatgtgta	ccttcagggg	cccatctggg	3180
	caaagattco	: acacacggac	ggacattttc	acccctctcc	cctcatgggt	ggattcggac	3240
50	ttaaacacco	tcctccacag	attctcatca	agaacacccc	ggtacctgcg	aatccttcga	3300
	ccaccttcag	tgcggcaaag	tttgcttcct	tcatcacaca	gtactccacg	ggacaggtca	3360
55	gcgtggagat	cgagtgggag	r ctgcagaagg	aaaacagcaa	acgetggaat	cccgaaattc	3420
	agtacactto	caactacaac	: aagtctgtta	atgtggactt	: tactgtggac	: actaatggcg	3.480
	tgtattcaga	a gcctcgcccc	attggcacca	gatacctgad	: tcgtaatctg	taattgcttg	3540
60	ttaatcaata	a aaccgtttaa	ttcgtttcag	, ttga			3574

<210> 6

<2	1	1>	31	2
_	_	_		

- <212> PRT
- <213> adeno-associated virus 2
- 5 <400> 6
 - Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1 $$ 5
- Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30
- 15 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 45
- Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 20 50 60
- Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
 - Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95
- Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
- Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125
- Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140
- Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160
 - Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175
- Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
- 55 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
- Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 60 210 215 220
 - Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235

-13-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 5 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 10 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 15 Arg Leu Ala Arg Gly His Ser Leu 305 310 20 <210> 7 <211> 397
<212> PRT
<213> adeno-associated virus 2 <400> 7 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1 5 10 15 30 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 35 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 50 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 11055 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 60

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

	Cys 145	Val	Asp	Lys	Met	Val 150	Ile	Trp	Trp	Glu	Glu 155	Gly	Lys	Met	Thr	Ala 160
5	Lys	Val	Val	Glu	Ser 165	Ala	Lys	Ala	Ile	Leu 170	Gly	Gly	Ser	Lys	Val 175	Arg
10	Val	Asp	Gln	Lys 180	Суз	Lys	Ser	Ser	Ala 185	Gln	Ile	Asp	Pro	Thr 190	Pro	Val
L5	Ile	Val	Thr 195	Ser	Asn	Thr	Asn	Met 200	Cys	Ala	Val	Ile	Asp 205	Gly	Asn	Ser
20	Thr	Thr 210	Phe	Glu	His	Gln	Gln 215	Pro	Leu	Gln	Asp	Arg 220	Met	Phe	Lys	Phe
	G1u 225	Leu	Thr	Arg	Arg	Leu 230	Asp	His	Asp	Phe	Gly 235	Lys	Val	Thr	Lys	Gln 240
25	Glu	Val	Lys	Asp	Phe 245	Phe	Arg	Trp	Ala	Lys 250	Asp	His	Val	Val	Glu 255	Val
30	Glu	His	Glu	Phe 260	Tyr	Val	Lys	Lys	Gly 265	Gly	Ala	Lys	Lys	Arg 270	Pro	Ala
35	Pro	Ser	Asp 275	Ala	Asp	Ile	Ser	Glu 280	Pro	Lys	Arg	Val	Arg 285	Glu	Ser	Val
10	Ala	Gln 290	Pro	Ser	Thr	Ser	Asp 295	Ala	Glu	Ala	Ser	Ile 300	Asn	Tyr	Ala	Asp
	Arg 305	Tyr	Gln	Asn	Lys	Cys 310	Ser	Arg	His	Val	Gly 315	Met	Asn	Leu	Met	Leu 320
15	Phe	Pro	Суз	Arg	Gln 325	Сув	Glu	Arg	Met	Asn 330	Gln	Asn	Ser	Asn	Ile 335	Cys
50	Phe	Thr	His	Gly 340	Gln	Lys	Asp	Cys	Leu 345	Glu	Суз	Phe	Pro	Val 350	Ser	Glu
55	Ser	Gln	Pro 355	Val	Ser	Val	Val	160 360	Lys	Ala	Tyr	Gln	Lys 365	Leu	Суз	Тут
50	Ile	His 370	His	Ile	Met	Gly	Lys 375	Val	Pro	Asp	Ala	Суs 380	Thr	Ala	Cys	Asp
	Leu 385	Val	Asn	Val	Asp	Leu 390	Asp	Asp	Cys	Ile	Phe 395	Glu	Gln			

8

<210>

2478 <211> <212> DNA adeno-associated virus 2 <400> 8 cagttgcgca gccatcgacg tcagacgcgg aagcttcgat caactacgca gacaggtacc 60 aaaacaaatg ttctcgtcac gtgggcatga atctgatgct gtttccctgc agacaatgcg 120 10 agagaatgaa tcagaattca aatatctgct tcactcacgg acagaaagac tgtttagagt 180 240 gctttcccgt gtcagaatct caacccgttt ctgtcgtcaa aaaggcgtat cagaaactgt 15 gctacattca tcatatcatg ggaaaggtgc cagacgcttg cactgcctgc gatctggtca 300 360 atgtggattt ggatgactgc atctttgaac aataaatgat ttaaatcagg tatggctgcc gatggttatc ttccagattg gctcgaggac actctctctg aaggaataag acagtggtgg 420 20 aagctcaaac ctggcccacc accaccaaag cccgcagagc ggcataagga cgacagcagg 480 540 ggtcttgtgc ttcctgggta caagtacctc ggacccttca acggactcga caagggagag 25 ccggtcaacg aggcagacgc cgcggccctc gagcacgaca aagcctacga ccggcagctc 600 gacageggag acaaceegta ceteaagtae aaceaegeeg aegeggagtt teaggagege 660 cttaaagaag atacgtcttt tgggggcaac ctcggacgag cagtcttcca ggcgaaaaag 720 30' agggttcttg aacctctggg cctggttgag gaacctgtta agacggctcc gggaaaaaag 780 aggccggtag agcactetee tgtggageca gacteeteet egggaacegg aaaggeggge 840 35 cagcagcctg caagaaaaag attgaatttt ggtcagactg gagacgcaga ctcagtacct 900 gacccccagc ctctcggaca gccaccagca gccccctctg gtctgggaac taatacgatg 960 gctacaggca gtggcgcacc aatggcagac aataacgagg gcgccgacgg agtgggtaat 1020 40 tcctcgggaa attggcattg cgattccaca tggatgggcg acagagtcat caccaccagc 1080 accegaacet gggecetgee cacetacaac aaccacetet acaaacaaat ttecagecaa 1140 45 1200 tcaggagcct cgaacgacaa tcactacttt ggctacagca ccccttgggg gtattttgac ttcaacagat tccactgcca cttttcacca cgtgactggc aaagactcat caacaacaac 1260 1320 tggggattcc gacccaagag actcaacttc aagctcttta acattcaagt caaagaggtc 50 acgcagaatg acggtacgac gacgattgcc aataacctta ccagcacggt tcaggtgttt 1380 1440 55 1500 ccgttcccag cagacgtctt catggtgcca cagtatggat acctcaccct gaacaacggg agtcaggcag taggacgctc ttcattttac tgcctggagt actttccttc tcagatgctg 1560 cgtaccggaa acaactttac cttcagctac acttttgagg acgttccttt ccacagcagc 1620 60 tacgctcaca gccagagtct ggaccgtctc atgaatcctc tcatcgacca gtacctgtat 1680 tacttgagca gaacaaacac tccaagtgga accaccacgc agtcaaggct tcagttttct 1740

	caggccggag cgagtgacat tcgggaccag tctaggaact ggcttcctgg accetgttac	1800
_	cgccagcagc gagtatcaaa gacatctgcg gataacaaca acagtgaata ctcgtggact	1860
5	ggagctacca agtaccacct caatggcaga gactctctgg tgaatccggg cccggccatg	1920
	gcaagccaca aggacgatga agaaaagttt tttcctcaga gcggggttct catctttggg	1980
10	aagcaaggct cagagaaaac aaatgtggac attgaaaagg tcatgattac agacgaagag	2040
	gaaatcagga caaccaatcc cgtggctacg gagcagtatg gttctgtatc taccaacctc	2100
4-	cagagaggca acagacaagc agctaccgca gatgtcaaca cacaaggcgt tcttccaggc	2160
15	atggtctggc aggacagaga tgtgtacctt caggggccca tctgggcaaa gattccacac	2220
	acggacggac attttcaccc ctctcccctc atgggtggat tcggacttaa acaccctcct	2280
20	ccacagattc tcatcaagaa caccccggta cctgcgaatc cttcgaccac cttcagtgcg	2340
	gcaaagtttg cttccttcat cacacagtac tccacgggac aggtcagcgt ggagatcgag	2400
0.5	tgggagctgc agaaggaaaa cagcaaacgc tggaatcccg aaattcagta cacttccaac	2460
25	tacaacaagt ctgttaat	2478
30	<210> 9 <211> 735 <212> PRT <213> adeno-associated virus 2	
35	<400> 9	
ن	Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser 1 10 15	
40	Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro 20 25 30	
45	Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro 35 40 45	
	Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro 50 55 60	

50

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp 65 70 75

55 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala 85

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly 100 105 105 11060

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg 130 135 140 5 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly 10 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr 165 170 17515 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly 20 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser 25 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile 225 230 235 240 30 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 35 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr 260 265 270 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His 275 280 285 40 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp 45 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val 50 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu 55 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser

370	375	380
-----	-----	-----

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser 5 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu 10 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg 15 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln 20 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly 25 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn 30 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly 500 510 35 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys 530 535 54040 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr 45 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr 50 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr 55 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr 610 620 60

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys

									٠							
	625					630					635					640
5	His	Pro	Pro	Pro	Gln 645	Ile	Leu	Ile	Lys	Asn 650	Thr	Pro	Val	Pro	Ala 655	Asn
LO	Pro	Ser	Thr	Thr 660	Phe	Ser	Ala	Ala	Lys 665	Phe	Ala	Ser	Phe	Ile 670	Thr	Gln
	Tyr	Ser	Thr 675	Gly	Gln	Val	Ser	Val 680	Glu	Ile	Glu	Trp	Glu 685	Leu	Gln	Lys
L5	Glu	Asn 690	Ser	Lys	Arg	Trp	Asn 695	Pro	Glu	Ile	Gln	Туг 700	Thr	Ser	Asn	Tyr
20	Asn 705	Lys	Ser	Val	Asn	Val 710	Asp	Phe	Thr	Val	Asp 715	Thr	Asn	Gly	Val	Туг 720
25	Ser	Glu	Pro	Arg	Pro 725	Ile	Gly	Thr	Arg	Tyr 730	Leu	Thr	Arg	Asn	Leu 735	
30	<210 <211 <211 <213	L> 5 2> E	0 598 PRT adeno	o-ass	socia	ated	vir	ıs 2								
	<400)> 1	LO													
35	Met 1	Ala	Pro	Gly	Lys 5	Lys	Arg	Pro	Val	Glu 10	His	Ser	Pro	Val	Glu 15	Pro
40	Asp	Ser	Ser	Ser 20	Gly	Thr	Gly	Lys	Ala 25	Gly	Gln	Gln	Pro	Ala 30	Arg	Lys
45	Arg	Leu	Asn 35	Phe	Gly	Gln	Thr	Gly 40	Asp	Ala	Asp	Ser	Val 45	Pro	Asp	Pro
	Gln	Pro 50	Leu	Gly	Gln	Pro	Pro 55	Ala	Ala	Pro	Ser	Gly 60	Leu	Gly	Thr	Asn
50	Thr 65	Met	Ala	Thr	Gly	Ser 70	Gly	Ala	Pro	Met	Ala 75	Asp	Asn	Asn	Glu	Gly 80
55	Ala	Asp	Gly	Val	Gly 85	Asn	Ser	Ser	Gly	Asn 90	Trp	His	Cys	Asp	Ser 95	Thr
60	Trp	Met	Gly	Asp 100	Arg	Val	Ile	Thr	Thr 105	Ser	Thr	Arg	Thr	Trp 110	Ala	Leu
	Pro	Thr	Tyr 115	Asn	Asn	His	Leu	Tyr 120	Lys	Gln	Ile	Ser	Ser 125	Gln	Ser	Gly

PCT/US03/01624

WO 03/061582

5	Ala	Ser 130	Asn	Asp	Asn	His	Tyr 135	Phe	Gly	Tyr	Ser	Thr 140	Pro	Trp	Gly	Tyr
	Phe 145	Asp	Phe	Asn	Arg	Phe 150	His	Cys	His	Phe	Ser 155	Pro	Arg	Asp	Trp	Gln 160
10	Arg	Leu	Ile	Asn	Asn 165	Asn	Trp	Gly	Phe	Arg 170	Pro	Lys	Arg	Leu	Asn 175	Phe
15	Lys	Leu	Phe	Asn 180	Ile	Gln	Val	Lys	Glu 185	Val	Thr	Gln	Asn	Asp 190	Gly	Thr
20	Thr	Thr	Ile 195	Ala	Asn	Asn	Leu	Thr 200	Ser	Thr	Val	Gln	Val 205	Phe	Thr	Asp
25	Ser	Glu 210	Tyr	Gln	Leu	Pro	Tyr 215	Val	Leu	Gly	Ser	Ala 220	His	Gln	Gly	Cys
	Leu 225	Pro	Pro	Phe	Pro	Ala 230	Asp	Val	Phe	Met	Val 235	Pro	Gln	Tyr	Gly	Tyr 240
30	Leu	Thr	Leu	Asn	Asn 245	Gly	Ser	Gln	Ala	Val 250	Gly	Arg	Ser	Ser	Phe 255	Tyr
35	Cys	Leu	Glu	Туг 260	Phe	Pro	Ser	Gln	Met 265	Leu	Arg	Thr	Gly	Asn 270	Asn	Phe
40	Thr	Phe	Ser 275	Туr	Thr	Phe	Glu	Asp 280	Val	Pro	Phe	His	Ser 285	Ser	Tyr	Ala
45	His	Ser 290	Gln	Ser	Leu	Asp	Arg 295	Leu	Met	Asn	Pro	Leu 300	Ile	Asp	Gln	Tyr
	Leu 305	Tyr	Tyr	Leu	Ser	Arg 310	Thr	Asn	Thr	Pro	Ser 315	Gly	Thr	Thr	Thr	Gln 320
50	Ser	Arg	Leu	Gln	Phe 325	Ser	Gln	Ala	Gly	Ala 330	Ser	Asp	Ile	Arg	Asp 335	Gln
55	Ser	Arg	Asn	Trp 340	Leu	Pro	Gly	Pro	Cys 345	Tyr	Arg	Gln	Gln	Arg 350	Val	Ser
60	Lys	Thr	Ser 355	Ala	Asp	Asn	Àsn	Asn 360	Ser	Glu	Tyr	Ser	Trp 365	Thr	Gly	Ala
	Thr	Lys 370		His	Leu	Asn	Gly 375	Arg	Asp	Ser	Leu	Val 380		Pro	Gly	Pro

	Ala 385	Met	Ala	Ser	His	390	Asp	Asp	GIU	GIU	395	Pne	Pne	Pro	GIN	400
	Gly	Val	Leu	Ile	Phe 405	Gly	Lys	Gln	Gly	Ser 410	Glu	Lys	Thr	Asn	Val 415	Asp
10	Ile	Glu	Lys	Val 420	Met	Ile	Thr	Asp	Glu 425	Glu	Glu	Ile	Arg	Thr 430	Thr	Asn
15	Pro	Val	Ala 435	Thr	Glu	Gln	Tyr	Gly 440	Ser	Val	Ser	Thr	Asn 445	Leu	Gln	Arg
20	Gly	Asn 450	Arg	Gln	Ala	Ala	Thr 455	Ala	Asp	Val	Asn	Thr 460	Gln	Gly	Val	Leu
25	Pro 465	Gly	Met	Val	Trp	Gln 470	Asp	Arg	Asp	Val	Tyr 475	Leu	Gln	Gly	Pro	Ile 480
	Trp	Ala	Lys	Ile	Pro 485	His	Thr	Asp	Gly	His 490	Phe	His	Pro	Ser	Pro 495	Leu
30	Met	Gly	Gly	Phe 500	Gly	Leu	Lys	His	Pro 505	Pro	Pro	Gln	Ile	Leu 510	Ile	Lys
35	Asn	Thr	Pro 515	Val	Pro	Ala	Asn	Pro 520	Ser	Thr	Thr	Phe	Ser 525	Ala	Ala	Lys
40	Phe	Ala 530	Ser	Phe	Ile	Thr	Gln 535	Tyr	Ser	Thr	Gly	Gln 540	Val	Ser	Val	Glu
45	Ile 545	Glu	Trp	Glu	Leu	Gln 550	Lys	Glu	Asn	Ser	L ys 555	Arg	Trp	Asn	Pro	Glu 560
	Ile	Gln	Tyr	Thr	Ser 565	Asn	Tyr	Asn	Lys	Ser 570	Val	Asn	Val	Asp	Phe 575	Thr
50	Val	Asp	Thr	Asn 580	Gly	Val	Tyr	Ser	Glu 585	Pro	Arg	Pro	Ile	Gly 590	Thr	Arg
55	Tyr	Leu	Thr 595	Arg	Asn	Leu										
60	<21 <21 <21 <21	1>. 2>	11 533 PRT aden	o-as	soci	ated	vir	us 2								•
	<40	0>	11													

	Met 1	Ala	Thr	Gly	Ser 5	Gly	Ala	Pro	Met	Ala 10	Asp	Asn	Asn	Glu	Gly 15	Ala
5	Asp	Gly	Val	Gly 20	Asn	Ser	Ser	Gly	Asn 25	Trp	His	Cys	Asp	Ser 30	Thr	Trp
10	Met	Gly	Asp 35	Arg	Val	Ile	Thr	Thr 40	Ser	Thr	Arg	Thr	Trp 45	Ala	Leu	Pro
15	Thr	Tyr 50	Asn	Asn	His	Leu	Tyr 55	Lys	Gln	Ile	Ser	Ser 60	Gln	Ser	Gly	Ala
20	Ser 65	Asn	Asp	Asn	His	Tyr 70	Phe	Gly	Tyr	Ser	Thr 75	Pro	Trp	Gly	Tyr	Phe 80
	Asp	Phe	Asn	Arg	Phe 85	His	Суз	His	Phe	Ser 90	Pro	Arg	Asp	Trp	Gln 95	Arg
25	Leu	Ile	Asn	Asn 100	Asn	Trp	Gly	Phe	Arg 105	Pro	Lys	Arg	Leu	Asn 110	Phe	Lys
30	Leu	Phe	Asn 115	Ile	Gln	Val	Lys	Glu 120	Val	Thr	Gln	Asn	Asp 125	Gly	Thr	Thr
35	Thr	Ile 130	Ala	Asn	Asn	Leu	Thr 135	Ser	Thr	Val	Gln	Val 140	Phe	Thr	Asp	Ser
40	Glu 145	Tyr	,Gln	Leu	Pro	Tyr 150	Val	Leu	Gly	Ser	Ala 155	His	Gln	Gly	Cys	Leu 160
	Pro	Pro	Phe	Pro	Ala 165	Asp	Val	Phe	Met	Val 170	Pro	Gln	Tyr	Gly	Tyr 175	Leu
45	Thr	Leu	Asn	Asn 180	Gly	Ser	Gln	Ala	Val 185	Gly	Arg	Ser	Ser	Phe 190	Tyr	Суз
50	Leu	Glu	Туг 195	Phe	Pro	Ser	Gln	Met 200	Leu	Arg	Thr	Gly	Asn 205	Asn	Phe	Thr
55	Phe	Ser 210	Tyr	Thr	Phe	Glu	Asp 215	Val	Pro	Phe	His	Ser 220	Ser	Tyr	Ala	His
60	Ser 225	Gln	Ser	Leu	Asp	Arg 230	Leu	Met	Asn	Pro	Leu 235	Ile	Asp	Gln	Tyr	Leu 240
	Tyr	Tyr	Leu	Ser	Arg 245	Thr	Asn	Thr	Pro	Ser 250		Thr	Thr	Thr	Gln 255	Ser

	Arg	Leu	Gln	Phe 260	Ser	Gln	Ala	Gly	Ala 265	Ser	Asp	Ile	Arg	Asp 270	Gln	Ser
5	Arg	Asn	Trp 275	Leu '	Pro	Gly	Pro	Суs 280	Tyr	Arg	Gln	Gln	Arg 285	Val	Ser	Lys
10	Thr	Ser 290	Ala	Asp	Asn	Asn	Asn 295	Ser	Glu	Tyr	Ser	Trp 300	Thr	Gly	Ala	Thr
15	Lys 305	Tyr	His	Leu	Asn	Gly 310	Arg	Asp	Ser	Leu	Val 315	Asn	Pro	Gly	Pro	Ala 320
20	Met	Ala	Ser	His	Lys 325	Asp	Ąsp	Glu	Glu	Lys 330	Phe	Phe	Pro	Gln	Ser 335	Gly
Δ	Val	Leu	Ile	Phe 340	Gly	Lys	Gln	Gly	Ser 345	Glu	Lys	Thr	Asn	Val 350	Asp	Ile
25	Glu	Lys	Val 355	Met	Ile	Thr	Asp	Glu 360	Glu	Glu	Ile	Arg	Thr 365	Thr	Asn	Pro
30	Val	Ala 370	Thr	Glu	Gln	Tyr	Gly 375	Ser	Val	Ser	Thr	Asn 380	Leu	Gln	Arg	Gly
35	Asn 385	Arg	Gln	Ala	Ala	Thr 390	Ala	Asp	Val	Asn	Thr 395	Gln	Gly	Val	Leu	Pro 400
40	Gly	Met	Val	Trp	Gln 405	Asp	Arg	Asp	Val	Tyr 410	Leu	Gln	Gly	Pro	Ile 415	Trp
	Ala	Lys	Ile	Pro 420	His	Thr	Asp	Gly	His 425	Phe	His	Pro	Ser	Pro 430	Leu	Met
45	Gly	Gly	Phe 435	Gly	Leu	Lys	His	Pro 440	Pro	Pro	Gln	Ile	Leu 445	Ile	Lys	Asn
50	Thr	Pro 450	Val	Pro	Ala	Asn	Pro 455	Ser	Thr	Thr	Phe	Ser 460	Ala	Ala	Lys	Phe
55	Ala 465	Ser	Phe	Ile	Thr	Gln 470	Tyr	Ser	Thr	Gly	Gln 475	Val	Ser	Val	Glu	Ile 480
60	Glu	Trp	Glu	Leu	Gln 485	Lys	Glu	Asn	Ser	Lys 490	Arg	Trp	Asn	Pro	Glu 495	Ile
	Gln	Tyr	Thr	Ser 500	Asn	Tyr	Asn	Lys	Ser 505	Val	Asn	Val	Asp	Phe 510	Thr	Val

Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr 515 520 5 Leu Thr Arg Asn Leu 530 10 <210> 12 <211> 145 <212> DNA <213> adeno-associated virus 2 15 <400> 12 ttggccactc cetetetgeg egetegeteg etcactgagg eegggegace aaaggtegee 60 120 cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 20 gccaactcca tcactagggg ttcct 145 <210> 13 <211> 144 25 <212> DNA <213> adeno-associated virus 2 ggaaccccta gtgatggagt tggccactcc ctctctgcgc gctcgctcgc tcactgaggc 30 egggegacca aaggtegeee gaegeeeggg etttgeeegg geggeeteag tgagegageg. 120 144 agcgcgcaga gagggagtgg ccaa 35 <210> 14 <211> 31 <212> DNA <213> adeno-associated virus 40 <220> <221> misc_feature <222> (1)..(31)<223> corresponds to base pairs 318-339 of AAV with an EcoR V site at 45 the 5' end <400> 14 31 gatatcgcca tgccggggtt ttacgagatt g 50 <210> 15 <211> 35 <212> DNA <213> adeno-associated virus 55 <220> <221> misc_feature <222> (1)..(35) 60 <223> corresponds to base pairs 1812 to 1846 of AAV <220> <221> mutation

```
<222> (20)..(20)
     <220>
     <221> mutation
    <222> (23)..(23)
     <400> 15
     gcacccgttt gggctcactg atgtctgcgt cactg
                                                                            35
10
     <210> 16
    <211> 35
<212> DNA
     <213> adeno-associated virus
15
     <220>
    <221> misc_feature
<222> (1)..(35)
20
    <223> corresponds to base pairs 1812 to 1846 of AAV
     <220>
     <221> mutation
     <222> (13)..(13)
25
     <220>
     <221> mutation
     <222> (16)..(16)
30
    <400> 16
                                                                            35
    cagtgacgca gacatcagtg agcccaaacg ggtgc
    <210> 17
35
    <211> 29
    <212> DNA
     <213> adeno-associated virus
40
    <220>
     <221> misc_feature
    <222> (1)..(29)
     <223> corresponds to base pairs 2261 to 2289 of AAV
45
    <400> 17
    tgggccaggt ttgagcttcc accactgtc
                                                                            29
    <210> 18
<211> 55
50
    <212> DNA
    <213> adeno-associated virus
55
    <220>
    <221> misc_feature
    <222> (1)..(27)
    <223> corresponds to base pairs 2261-2289 of AAV
    <220>
60
    <221> misc_feature
    <222> (28)..(53)
    <223> corresponds to base pairs 4330-4355 of AAV
```

PCT/US03/01624

WO 03/061582

WO 03/061582 PCT/US03/01624 <400> 18 gacagtggtg gaagctcaaa cctggcccaa gcacctgaat ggcacctatg attac 55 <210> 19 <211> 28 <212> DNA <213> adeno-associated virus 10 <220> <221> misc_feature <222> (1)..(28) <223> corresponds to base pairs 4446-4467 of AAV with a BamHI site at 15 the 3' end <400> 19 ggatcccgca gagaccaaag ttcaactg 28 20 <210> 20 <211> 27 <212> DNA <213> adeno-associated virus 25 <220> <221> misc_feature <222> (1)..(27) 30 <223> corresponds to base pairs 1852 to 1878, BamHI site at the 5' end <400> 20 agtcagttgc gcagccatcg acgtcag 27 35 <210> <211> 35 <212> DNA <213> adeno-associated virus 40 <220> <221> misc_feature <222> (1)..(35) 45 <223> corresponds to base pairs 4302 to 4329, with a Not I site at the 3' end

<210> 22
<211> 592
<212> DNA

55 <213> Homo sapiens

<400> 22
gcgtgaagag ctgcagtgtc actcttaaag ctgaattaat ctctgccatt ccttaaggaa 60

acaggcaact gtcttaaaac cgtggtttgg aaaatattt gttcaagata aaactgtttt 120
aagatatatg tatatatatc ttatatatct gtattcgcat ggtaacatat cttcggtctt 180
cctgccgctg ggctctcagc ggccctcaa ggcagcccgc aggcccgtgc tcgcctcagg 240

35

<400> 21

50

gcggccgctt aacagacttg ttgtagttgg aagtg

	gatcctccac	agccccgggg	agaccttgcc	tctaaagttg	ctgcttttgc	agctctgcca	300
5	caaccgcgcg	tcctcagagc	cagccgggag	gagctagaac	cttccccgcg	tttctttcag	360
•	cagccctgag	tcagaggcgg	gctggccttg	caagtagccg	cccagccttc	ttcggtctca	420
	cggaccgatc	cgcccgaacc	ttctcccggg	gtcagcgccg	cgctgcgccg	cccggctgac	480
10	tcagcccggg	cgggcgggcg	ggaggctctc	gactgggcgg	gaaggtgcgg	gaaggttcgc	540
	ggcggcgggg	tcggggaggt	gcaaaaggat	gaaaagcccg	tagacagage	ta	592